

A14

1 GCGTAATCT GCTGCTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT  
51 TTGTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT  
101 CAGCAGAGCG CAGATACCAA ATACTGTCT TCTAGTGTAG CCGTAGTTAG  
151 GCCACCACCT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA  
201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG  
251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA  
301 CGGGGGGTTTC GTGCACACAG CCCAGCTTGG AGCCAACGAC CTACACCGAA  
351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGGCCACGC TTCCCGAAGG  
401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC  
451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTA TAGCCTGTC  
501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTTGTGAT GTCGTCAAGG  
551 GGGGCGGAGC CTATGGAAA ACGCCAGCAA CGCCGAATTAA CGCGGTCTT  
601 TCTCAACGTA ACACTTACA GCGGGCGCTC ATTTGATATG ATGCGCCCG  
651 CTTCCCGATA AGGGAGCAGG CCAGTAAAG CATTACCCGT GGTGGGGTTC  
701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTAT CGACTTCGAA  
751 GGTTCGAATC CTTCCCCAC CACCATCACT TTCAAAAGTC CGAAAGAATC  
801 TGCTCCCTGC TTGTGTGTTG GAGGTGGCTG AGTAGTGCAG GAGTAAAATT  
851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGATGA AGAATCTGCT  
901 TAGGGTTAGG CGTTTGCAG TGCTTCGCGA TGACGGGCC AGATATAACG  
951 GTTGACATTG ATTATTGACT AGTTATTAAAT AGTAATCAAT TACGGGGTCA  
1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAA  
1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATGG ACGTCAATAA  
1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA  
1151 TGGGTGGACT ATTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGT  
1201 TCATATGCCA AGTACGCCCG CTATTGACGT CAATGACGGT AAATGGCCCG  
1251 CCTGGCATTAA TGCCCAAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG  
1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGTGATGC GGTTTTGGCA  
1351 GTACATCAAT GGGCGTGGAT AGCGGTTGA CTCACGGGGA TTTCCAAGTC  
1401 TCCACCCCAT TGACGTCAAT GGGAGTTGT TTTGGCACCA AAATCAACGG  
1451 GACTTTCAA AATGTGTAA CAACTCCGCC CCATTGACGC AAATGGCCGG  
1501 AATTCCCTGGG CGGGACTGGG GAGTGGCGAG CCCTCAGATG CTGCATATAA  
1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG  
1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACCC CACTGCTTAA GCCTCAATAA  
1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGGA TCTTCCATAC CTACCAAGTTC

FIG. 1A

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1701 TCGGCCTGCA GGTCCGGGCC QCGACTCTAG AGGATCTTG TGAAGGAACC  
1751 TTACTTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA  
1801 GCTCTAAGGT AAATATAAAA TTTTAAGTG TATAATGTGT TAAACTACTG  
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG  
1901 GGAGCAGTGG TGGAATGCCT TTAATGAGGA AAACCTGTT TGCTCAGAAG  
1951 AAATGCCATC TAGTGTGAT GAGGCTACTG CTGACTCTCA ACATTCTACT  
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCCTTCAGA  
2051 ATTGCTAAGT TTTTGAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT  
2101 GCTTGCTAT TTACACCACA AAGGAAAAG CTGCACTGCT ATACAAGAAA  
2151 ATTATGGAAA AATATTCTGT AACCTTATA AGTAGGCATA ACAGTTATAA  
2201 TCATAACATA CTGTTTTTC TTACTCCACA CAGGCATAGA GTGTCTGCTA  
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTT AATTTGTAAA  
2301 GGGGTTAATA AGGAATATTG GATGTATAGT GCCTTGACTA GAGATCATAA  
2351 TCAGCCATAC CACATTGTA GAGGTTTAC TTGCTTTAAA AAACCTCCCA  
2401 CACCTCCCCC TGAAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTTAA  
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA  
2501 ATTTCACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TCGTTTGTCC  
2551 AAACTCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA  
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAA  
2651 GCATGCATCT CAATFAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC  
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT  
2751 AGTCCCCGCC CTAACCTCCGC CCATCCCCGC CCTAACTCCG CCCAGTTCCG  
2801 CCCATTCTCC GCCCCATGGC TGACTAAATT TTTTTATTTA TGCAAGAGGCC  
2851 GAGGCCGCCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTT  
2901 TGGAGGCCTA GGCTTTGCA AAAAGCTAAT TC

FIG. 1B

Cont  
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CCTAAGATGAGCTTCCATGTAAATTGTAGCCAGCTTCCCTGATTTCATGTTCT  
METSERPHEPROCYSLYSPHEVALALASERPHELEUILEPHEASNVALSER (60)  
TCCAAAGGTGAGTCTCCAAGAGATTACGAATGCCCTGGAAACCTGGGTGCCCTGGT  
SERLYSGLYALAVALSERLYSGLUILETHRASNALALEUGLUTHRPGLYALALEUGLY (120)  
CAGGACATCAGTGGACATTCTAGTTCAAATGAGTGTGATATTGACGATATAAA  
GLNAPILEASNLEUAPILEPROSERPHEGLNMETSERASPAPILEASPAPILELYS (180)  
TGGGAAAAAACTTCAGACAAGAAAAGATTGACAAATTCAAGAAAAGAGAAAGAGACTTCT  
TRPGLULYSTHRSEASPLYSLYSILEALAGLNPIHEARGLYSGLUYSGLUTHRPHE (240)  
AAGGAAAAAACTACATATAAGCTATTAAAGAACTGAACTCTGAAAATTAAAGCATCTGAAAG (300)  
LYSGLUYSASPTHR TYRLYSLEUPHELYSNGLYTHRLEULYSILELYSHISLEULYS  
---CHO--- (360)  
ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAGGAAAGAAATGTGTTG  
THRASPAPGLNAPILETYRLYSVALSERILETYRASPTHRYSGLYLYSASNVALLEU (420)  
GAAAAAAATTGATTGAAAGATTCAAGAAGGGTCTCAAAACCAAAGATCTCCTGGACT  
GLULYSILEPHEASPLEULYSILEGLNGLUARGVALSERLYSProLYSILESERTRPTHR (480)  
TGTATCAACACAACCCCTGACCTGTGAGGTAACTGAATGGAACCTGACCCCGAATTAAACCTG  
CYSILEASNTHRLEUTHRCSGLUVALMETASNGLYTHRASPPIROGLULEUASNLEU  
---CHO--- (540)  
TATCAAGATGGAAACATCTAAAACCTTCTCAGAGGGTCATCACACACAAGTGGACCAC  
TYRGLNAPGLYLYSHISLEULYSLEUSERGLNARGVALILETHRHSLYSTRPTHRTHR (600)  
AGCCTGAGTGCAGGAACTCAAGTGCACAGCAGGAACAAAGTCAGCAAGGAATCCAGTGT  
SERLEUSERALALYSPELYSCYSTHRALAGLYASNLYSVALSERLYSGLUSERSERVAL (660)  
GAGCCTGTCAGCTGTCCAGAGAAAAGGTCTGGACATCTATCTCATCATGGCATATGTGG  
GLUPROVALSERCYSProGLULYSGLYLEUAPILETYRLEUILEILEGLYILECYSGLY (720)  
GGAGGCAGCCCTTGTGGCTTGTGGCAGTGTGCTCGTTCTATATCACCAAAAGGAA  
GLYGLYSERLEULEUMETVALPHEVALALALEUVALPHETYRILETHRYSARGLYS  
---TM--- (780)  
AAACAGAGGAGTCGGAGAAAATGATGAGGGAGCTGGAGACAAGAGCCCACAGACTAGCTACT  
LYSGLNARGSERARGARGASNAPGLUGLUUGLUTHRARGVALALATHR (840)  
GAAGAAAGGGCCGGAAGCAGCCAAACAAATTCCAGCTCAACCCCTCAGAACATCCAGCAACT  
GLUGLUARGGLYARGLYSProGLNILEPROALASERTHRPROGLNAPROALATHR (900)  
TCCCAACATCCTCCACACCTGGTCACTCGTCCAGGCACTAGTCATCGTCCCCG  
SERGLNHSProProProProProProGLYHISARGSERGLNAPROSERHISARGProPro (960)  
CCTCCTGGACACCGTGTCAAGCACCAGCTCAGAAGAGGCTCTGCTCCGTCGGGCAC  
ProProGLYHISARGVALGLNHSGLNPROGLNLYSARGPROPROALAPROSERGLYTHR

FIG. 2A

Copy  
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300 CAAGTTACCCAGCAGAAAGGCCGCCCCCTCCCCAGACCTCGAGTTAGCCAAAACCTCCG (1020)  
GLNVALHISGLNGLNLYSGLYPROPROLEU~~PRO~~ARGPRO~~ARG~~VALGLNPROLYS~~PRO~~PRO  
320 CATGGGGCA~~G~~CAGAAA~~A~~CT~~C~~ATTGTCCCC~~T~~TCCTCTAATTAAAAAAAGATAGAAACTGTCT (1080)  
HISGLYALAALAGL~~U~~AS~~N~~SERLEUSERPROSERSERAS~~N~~END  
TTTCAATAAAAA~~G~~CACTGTGGATTCTGCCCC~~T~~CTGATGTGCATATCCGTACTTCCATG (1140)  
AGGTGTTTCTGTGTGCAGAACATTGTCA~~C~~CTCCTGAGGCTGTGGGCCA~~C~~AGCCACCTCT (1200)  
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTGGTCTCCTCAGAGAGCTC (1260)  
CATCACACCAGTAAGGAGAACAA~~T~~ATAAGTGTGATTGCAGAATGGTAGAGGACCGAGC (1320)  
ACAGAAATCTAGAGATTCTGTCCCC~~T~~TCAGGT~~C~~ATGTGAGATGC~~G~~ATAAA~~T~~CAAG (1380)  
TGATTGGTG~~T~~GCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGA~~C~~TCTGGAGTT (1440)  
CTTATGTGCCTGGTGGAC~~A~~CTTGCCCCACCATCCTGTGA~~G~~TAAAGTGA~~A~~ATAAAAGCTT (1500)  
TGAC (1504)

**FIG. 2B**

1 GGC GTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT  
51 TTGTTTGCCTG GATCAAGAGC TACCAACTCT TTTCCGAAG GTAAGTGGCT  
101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTAA GCCGTAGTTA  
151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT  
201 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG  
251 GGTTGGACTC AAGACGATAG TTACCGATA AGGCGCAGCG GTCGGGCTGA  
301 ACGGGGGTT CGTGCACACA GCCCAGCTG GAGCGAACGA CCTACACCGA  
351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG  
401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCCG AACAGGAGAG  
451 CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGCCTGT  
501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG  
551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT  
601 AGAAATTGTA AACGTTAATA TTTTGTAAA ATTGCGTTA AATTTTTGTT  
651 AAATCAGCTC ATTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT  
701 AAATCAAAG AATAGCCCGA GATAGGGTTG AGTGTGTTTC CAGTTGGAA  
751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAA GGGCGAAAAAA  
801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA  
851 AGTTTTTG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG  
901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA  
951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCCGT GGCAAGTGTAA  
1001 GCGGTACGC TGCGCGTAAC CACCACACCC GCCCGCGTTA ATGCCCGCT  
1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCCTTCC

**FIG. 6A**

1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTT  
1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTC TCAACGTAAC  
1201 ACTTTACAGC GGCAGTCAT TTGATATGAT GCGCCCCGCT TCCCGATAAG  
1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGTTCCC GAGCGGCCAA  
1301 AGGGAGCAGA CTCTAAATCT GCCGTATCG ACTTCGAAGG TTCAATCCT  
1351 TCCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCCTGCTT  
1401 GTGTGTTGGA GGTGCTGAG TAGTGGCGA GTAAAATTAA AGCTACAACA  
1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG  
1501 TTTTGGCTG CTTGCGATG TACGGGCCAG ATATACGCGT TGACATTGAT  
1551 TATTGACTAG TTATTAATAG TAATCAATTAA CGGGGTCTT AGTTCATAGC  
1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCCCCCTGG  
1651 CTGACCGCCC AACGACCCCCC GCCCATTGAC GTCAATAATG ACGTATGTT  
1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT  
1751 TTACGGTAAA CTGCCCCTT GGCAGTACAT CAACTGTATC ATATGCAAG  
1801 TACGGCCCTT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG  
1851 CCCAGTACAT GACCTTATGG GACTTCCTA CTTGGCAGTA CATCTACGTA  
1901 TTAGTCATCG CTATTACCAT GGTGATGGGG TTTTGGCAGT ACATCAATGG  
1951 GCGTGGATAG CGGTTTGAAT CACGGGGATT TCCAAGTCTC CACCCATTG  
2001 ACGTCAATGG GAGTTTGTAA TGGCACCAAA ATCAACGGGA CTTTCCAAAA  
2051 TGTCGTAACA ACTCCGCCCTT ATTGACGCAA ATGGCCGGAA TTCCCTGGCG  
2101 GGACTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT  
2151 TGCCTGTACT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT  
2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCATAAAAG CTTCTAGAGA  
2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

**FIG. 6B**

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTCA AAGCATGACA  
2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTTAACGA  
2401 GGTGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGG  
2451 TTCAGCAGCC GGGCCTTAC TGGCACTTCA GGAAACAAGCG GGGCCTGCTC  
2501 GACGCAGTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTCGGTGCC  
2551 GAGAGCCGAC GACGACTGGC GCTCATTCT GACTGGGAAT GCCCCGACCT  
2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC  
2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGGCCGC GACTCTAGAG  
2701 GATCTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC  
2751 TACCTACAGA GATTAAAGC TCTAAGGTAA ATATAAAATT TTTAAGTGTAA  
2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC  
2851 CTATGGAAC-T-GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA  
2901 ACCTGTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT  
2951 GACTCTAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC  
3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTA  
3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GGAAAAAGCT  
3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG  
3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTCTT ACTCCACACA  
3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT  
3251 AGCTTTTAA TTTGTAAGG GGTTAATAAG GAATATTGA TGTATAGTGC  
3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTGTAGA GGTTTTACTT  
3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA  
3401 TGCAATTGTT GTTGTAACT TGTTATTGC AGCTTATAAT GGTTACAAAT  
3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTGTTT TTCACTGCAT

**FIG. 6C**

3501 TCTAG~~T~~TGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT  
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG  
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAAGGTGT  
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGAAA GCATGCATCT  
3701 CAATTAGTCA GCAACCATAG TCCCGCCCT AACTCCGCC ATCCCGCCCC  
3751 TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATT~~TTTT~~  
3801 TTTATTATG CAGAGGCCGA GGCCGCCCTCG GCCTCTGAGC TATTCCAGAA  
3851 GTAGTGAGGA GGCTTTTGTG GAGGCCTAGG CT~~TTTG~~CAAA AAGCTAATTG

**FIG. 6D**

AGACTCTCA~~G~~CCCTGGCAGGTGCGTCTT~~T~~CAGTCCCC~~T~~CACACTCGGGTTCTCGG~~G~~ (60)  
 GAGGAGGG~~G~~TGGAACCT~~A~~GCCATCGT~~C~~AGGACAAAG~~A~~GCTCAGG~~T~~GCTCTGG~~T~~ (120)  
 METLEU~~A~~RGLE~~U~~LEU~~U~~ALA  
 -18  
 CTCAACTTATTCCCTCAATTCAAGTAAC~~A~~GGAAACAAG~~A~~TTGGTGA~~A~~GCAGTCGCC~~C~~ (180)  
 LEU~~A~~SNLEU~~P~~HE~~P~~ROSER~~I~~LEGLNVAL~~T~~HRLYASNL~~S~~ILEU~~V~~ALLYSGLN~~S~~ER~~P~~RO  
 10 ATGCTTGT~~A~~CGTACGACA~~A~~TGGGTCAAC~~C~~TTAGCTG~~C~~AGTATTCT~~C~~ACAATCTCT~~T~~ (240)  
 METLEU~~V~~ALALA~~T~~YRASPASN~~A~~LAVAL~~S~~NLEU~~S~~ERCYS~~L~~YS~~T~~YRS~~E~~TYRASNLEU~~P~~HE  
 ---CHO---  
 30 TCAAGGGAG~~T~~CGGGCAT~~C~~CTCACAAAGGACTGG~~A~~GTGCTGTGG~~A~~GTCTGTG~~T~~ (300)  
 SERARG~~G~~LU~~P~~HE~~A~~RGALASERLEU~~H~~ISLYSGLYLEUASP~~S~~ER~~A~~LAVAL~~G~~LU~~V~~AL~~C~~YS~~V~~AL  
 50 GTATATGG~~A~~ATTACTCCC~~A~~GGAGCTTCAG~~T~~GGT~~A~~GT~~T~~ACTCA~~A~~AAACGGGG~~T~~CAACTGTG~~A~~ (360)  
 VAL~~T~~YRGLYASNL~~T~~YR~~S~~ERGLNGLNLEU~~G~~LNVAL~~T~~YR~~S~~ERLYS~~T~~YRGLY~~P~~HE~~A~~SN~~C~~YS~~A~~SP  
 ---CHO---  
 70 GGGAAATTGG~~G~~CAATGAAT~~C~~AGTGACATT~~C~~ACCTCCAG~~A~~ATT~~T~~GTATG~~T~~TAACCAAAC~~A~~ (420)  
 GLYLYSLEU~~G~~LYASNL~~U~~SERVAL~~T~~H~~R~~P~~H~~E~~T~~YR~~L~~E~~U~~GN~~N~~LEU~~T~~YR~~V~~AL~~A~~SN~~G~~LN~~T~~HR  
 ---CHO---  
 90 GATATTACTCTG~~C~~AAAATTGAAGTTAT~~G~~TATCCTCCT~~C~~TTACCTAG~~A~~CAATGAGAAG~~A~~ (480)  
 ASP~~I~~LET~~T~~YR~~P~~HE~~C~~YS~~L~~YS~~I~~LEGLU~~V~~AL~~M~~ET~~T~~YR~~P~~RO~~P~~RO~~P~~RO~~T~~YR~~L~~E~~U~~ASP~~A~~SN~~G~~L~~U~~YS  
 110 AGCAATGGAACCATTATCC~~A~~TGT~~G~~AAAGGGAAACAC~~C~~TT~~T~~GTCCAAGT~~C~~CCCTATTCC~~C~~ (540)  
 SERAS~~N~~GLY~~T~~HR~~I~~LE~~H~~IS~~V~~ALLYSGLYSHIS~~L~~EU~~C~~YS~~P~~ROSER~~P~~RO~~L~~U~~P~~HE~~P~~RO  
 ---CHO---  
 130 GGACCTCTAAGCCC~~T~~TTGGGTGCTGG~~T~~GGT~~G~~GTGG~~T~~GGAGTCTGG~~T~~TGCTATA~~G~~ (600)  
 GLY~~P~~ROSERLYS~~P~~RO~~H~~E~~T~~RP~~V~~ALLEU~~V~~AL~~V~~AL~~G~~LY~~G~~LY~~V~~ALLEU~~A~~CYS~~T~~YR~~S~~ER  
 ---TM---  
 150 TTGCTAGTA~~A~~CGTGGC~~T~~TTATTATT~~T~~GGGTGAGGAGTAAGAGGAGCAGG~~G~~CTCTG~~G~~ (660)  
 LEU~~E~~LU~~V~~AL~~T~~HR~~V~~AL~~A~~LA~~P~~HE~~I~~LE~~P~~HE~~T~~RP~~V~~AL~~A~~RG~~S~~ERLYS~~A~~RG~~S~~ER~~A~~RG~~L~~EU  
 170 CACAGTGA~~T~~ACATGAACATGACTCCCCGCC~~G~~CCCCGGG~~C~~CCACCCGA~~A~~GCATTACCA~~G~~ (720)  
 HIS~~S~~ERAS~~P~~TYR~~M~~ET~~A~~SN~~M~~ET~~T~~HR~~P~~RO~~A~~RG~~A~~RG~~P~~RO~~G~~LY~~P~~RO~~H~~R~~A~~GLY~~Y~~SHIS~~T~~YR~~G~~LN  
 190 CCCTATGCC~~C~~ACCACCGG~~A~~CTCGCAGC~~C~~TATCGCT~~C~~TGACACGGAC~~G~~CCTATCC~~G~~ (780)  
 PRO~~T~~YR~~A~~LA~~P~~RO~~P~~RO~~A~~RG~~A~~SP~~P~~HE~~A~~LA~~A~~LA~~T~~YR~~A~~RG~~S~~ER~~E~~ND  
 202.  
 AGCCAGCCGGCTGGCAGCC~~C~~CATCTGCT~~C~~AA~~T~~ATCACTGCTCTGG~~A~~AGGAAATGACCG (840)  
 CCATCTCCAGCCGGCCAC~~T~~CAGCCC~~T~~G~~T~~GGGCCACC~~A~~ATGCC~~A~~ATT~~T~~TCGAGT~~G~~ (900)  
 ACTAGACCA~~A~~ATCAAGA~~T~~CA~~T~~TTGAG~~A~~CTGAA~~A~~GT~~A~~AGTAAAAGAGATT~~T~~CCTGT~~T~~ (960)  
 GACAGGCCA~~A~~GTCTTACAG~~T~~GCCATGGCC~~C~~ACATTCAA~~C~~TTACCATGT~~A~~CTTAGT~~G~~ACT (1020)  
 TGACTGAGAAGTTAGGG~~A~~GAAAACAAAAGGGAGTGG~~A~~TTCTGGAGC~~T~~CTTCCCTT~~T~~ (1080)

**FIG. 7A**

CTCACTCACCTGCACATCTCAGTCAGCAAAAGTGTGGTATCCACAGACATTTAGTTGC (1140)  
GAAGAAAGGCTAGGAAATCATTCCCTTTGGTTAAATGGGTGTTAATCTTTGGTTAGTG (1200)  
GGTTAAACGGGGTAAGTTAGACTAGGGGGAGGGATAGGAAGACATATTTAAAAACCATT (1260)  
AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCTATTTAATGCTGTTTCCCT (1320)  
TAGTTAGAAATACATAGACATTGTCTTTATGAATTCTGATCATATTTAGTCATTG (1380)  
CCAAATGAGGGATTGGTCAAATGAGGGATTCCCTCAAAGCAATATCAGGAAACCAAGT (1440)  
TGCTTTCCCTCACTCCCTGTCACTGAGACTTCACTGTTAATGTTACAATAACTTTGAA (1500)  
GAATAAAATAGTTC (1514)

**FIG. 7B**

TAGACCCAGAGAGGGCTCAGCTGCACTCGC<sup>1</sup>CGCTGGAGAGCTGGGTG<sup>2</sup>GGGAACATG<sup>3</sup>  
 MET (60)

GCCGGGCCT<sup>1</sup>CGAGGCTCTGCTGCC<sup>2</sup>CTGCTGGCTGGCTCGGGCTGCC<sup>3</sup>  
 ALAGLYPROPROARGLEULEULEU<sup>4</sup>PROLEULEU<sup>5</sup>ALALEU<sup>6</sup>ALAARGGLYLEU<sup>7</sup>PRO  
 GLYALALEU<sup>8</sup>ALAALAGL<sup>9</sup> / (120)

TCTCCCTGCC<sup>1</sup>CATGAGCT<sup>2</sup>AGAGCCCC<sup>3</sup>AGTCTGAGCC<sup>4</sup>ACAGCACAGC<sup>5</sup>CCCCAGGAAGC<sup>6</sup>  
 GGGTGGGT<sup>7</sup>GCTGAGCGGC<sup>8</sup>CTCCAGTGT<sup>9</sup>CTGAGGACTCA<sup>10</sup>TTAAGAGAA<sup>11</sup>GGAAAAAGGT<sup>12</sup>  
 GGACCCGGT<sup>13</sup>GGGGACTGCC<sup>14</sup>GGGGCTGTC<sup>15</sup>AGGCAGGGC<sup>16</sup>CGCTGCT<sup>17</sup>TGGGAGGAAGAAG<sup>18</sup>  
 CCCACAGT<sup>19</sup>CGGAACACGGAGCAC<sup>20</sup>AC<sup>21</sup>CCCCAAC<sup>22</sup>ACCACAGCCGGT<sup>23</sup>GCCAGATC<sup>24</sup>  
 TGCTCCATGCC<sup>25</sup>GTAA<sup>26</sup>GGCACCGTGTCT<sup>27</sup>TGGGACAT<sup>28</sup>GT<sup>29</sup>CAGCCCTGGGCTGTCTCA<sup>30</sup>  
 GGCCCCACC<sup>31</sup>ATCCCCACCA<sup>32</sup>CTGTCCCCTG<sup>33</sup>AGGGAGGAC<sup>34</sup>ATTCTCTGTC<sup>35</sup>TTCTGGCCAG<sup>36</sup>  
 ACTGATGGT<sup>37</sup>GACAGCCCAGGT<sup>38</sup>CTCCCAGAGGT<sup>39</sup>GT<sup>40</sup>CA<sup>41</sup>GTCT<sup>42</sup>CC<sup>43</sup>CA<sup>44</sup>TC<sup>45</sup>GCACGACTGT<sup>46</sup>  
 GLU<sup>47</sup>VAL<sup>48</sup>GLN<sup>49</sup>GLN<sup>50</sup>SER<sup>51</sup>PRO<sup>52</sup>HIS<sup>53</sup>CYS<sup>54</sup>THR<sup>55</sup>THR<sup>56</sup>VA<sup>57</sup> (540)

CCCCGTGGGAGCCTCCGTC<sup>1</sup>AACATCACCT<sup>2</sup>GCTCCACCAGC<sup>3</sup>GGGGCCTG<sup>4</sup>GTGGGATCT<sup>5</sup>  
 L<sup>6</sup>PRO<sup>7</sup>VAL<sup>8</sup>GLY<sup>9</sup>ALA<sup>10</sup>SER<sup>11</sup>VAL<sup>12</sup>ASN<sup>13</sup>ILE<sup>14</sup>THR<sup>15</sup>CYS<sup>16</sup>SER<sup>17</sup>THR<sup>18</sup>SER<sup>19</sup>GLY<sup>20</sup>GLY<sup>21</sup>LEU<sup>22</sup>ARG<sup>23</sup>GLY<sup>24</sup>ILE<sup>25</sup>TY<sup>26</sup>---CHO--- (600)

CCTGAGGCA<sup>1</sup>GCTGGGCC<sup>2</sup>ACAGCCCCAAGACATCATT<sup>3</sup>TA<sup>4</sup>CTACGAGGAC<sup>5</sup>GGGTGGTGC<sup>6</sup>C  
 RLEU<sup>7</sup>ARG<sup>8</sup>GLN<sup>9</sup>LEUGLY<sup>10</sup>PROGLN<sup>11</sup>PROGLN<sup>12</sup>ASPILE<sup>13</sup>ILE<sup>14</sup>TY<sup>15</sup>TYR<sup>16</sup>GLU<sup>17</sup>ASP<sup>18</sup>GLY<sup>19</sup>VAL<sup>20</sup>VAL<sup>21</sup>PR<sup>22</sup>  
 CACTACGGACAGACGGTC<sup>1</sup>CGGGCCGCA<sup>2</sup>TCGACTTCTC<sup>3</sup>AGGGTCCC<sup>4</sup>AGGACAA<sup>5</sup>CTGA<sup>6</sup>  
 O<sup>7</sup>THR<sup>8</sup>THR<sup>9</sup>ASP<sup>10</sup>R<sup>11</sup>ARG<sup>12</sup>P<sup>13</sup>G<sup>14</sup>H<sup>15</sup>ARG<sup>16</sup>ILE<sup>17</sup>ASP<sup>18</sup>P<sup>19</sup>H<sup>20</sup>S<sup>21</sup>E<sup>22</sup>R<sup>23</sup>G<sup>24</sup>L<sup>25</sup>Y<sup>26</sup>---CHO--- (720)

TATCACCATGACCGCCTG<sup>1</sup>AGCTGTGG<sup>2</sup>ACACTGGCAC<sup>3</sup>TACACCTGC<sup>4</sup>AGGCCATCAC<sup>5</sup>  
 RILE<sup>6</sup>THR<sup>7</sup>METHIS<sup>8</sup>ARG<sup>9</sup>LEUGLN<sup>10</sup>LEU<sup>11</sup>SER<sup>12</sup>ASP<sup>13</sup>THR<sup>14</sup>GLY<sup>15</sup>THR<sup>16</sup>CYS<sup>17</sup>QLN<sup>18</sup>ALA<sup>19</sup>ILE<sup>20</sup>TH<sup>21</sup>  
 GGAGGTCAA<sup>1</sup>GTCTACGG<sup>2</sup>CTCCGGCACCC<sup>3</sup>GGTCTGGT<sup>4</sup>ACAGAGGAA<sup>5</sup>AGTCCC<sup>6</sup>AGG<sup>7</sup>  
 RGLU<sup>8</sup>VAL<sup>9</sup>AS<sup>10</sup>N<sup>11</sup>VAL<sup>12</sup>TYR<sup>13</sup>GLY<sup>14</sup>SER<sup>15</sup>GLY<sup>16</sup>THR<sup>17</sup>LEU<sup>18</sup>VAL<sup>19</sup>THR<sup>20</sup>GLU<sup>21</sup>GLU<sup>22</sup>LN<sup>23</sup>SER<sup>24</sup>GLN<sup>25</sup>  
 ATGGCACAGATGCTGGAC<sup>1</sup>CCCCACCA<sup>2</sup>AGGGCTCTGC<sup>3</sup>CC<sup>4</sup>CTCCCTGCC<sup>5</sup>CCACCGACAGG<sup>6</sup>  
 Y<sup>7</sup>TRPHIS<sup>8</sup>ARG<sup>9</sup>CYS<sup>10</sup>SER<sup>11</sup>ASP<sup>12</sup>ALA<sup>13</sup>PRO<sup>14</sup>PRO<sup>15</sup>ARG<sup>16</sup>ALA<sup>17</sup>LEU<sup>18</sup>PRO<sup>19</sup>ALA<sup>20</sup>PRO<sup>21</sup>PRO<sup>22</sup>THR<sup>23</sup>GL<sup>24</sup>  
 CTCCGCC<sup>1</sup>CTGCC<sup>2</sup>GTACCCG<sup>3</sup>AGACAGCC<sup>4</sup>CTGCC<sup>5</sup>CTCC<sup>6</sup>CTGACCCGCC<sup>7</sup>AGC<sup>8</sup>AGGCC<sup>9</sup>CTG<sup>10</sup>C  
 Y<sup>11</sup>SER<sup>12</sup>ALA<sup>13</sup>LEU<sup>14</sup>PRO<sup>15</sup>ASP<sup>16</sup>PRO<sup>17</sup>LN<sup>18</sup>THR<sup>19</sup>ALA<sup>20</sup>SER<sup>21</sup>ALA<sup>22</sup>LEU<sup>23</sup>PRO<sup>24</sup>ALA<sup>25</sup>ALA<sup>26</sup>SER<sup>27</sup>AL<sup>28</sup>Y<sup>29</sup>  
 CCTCCCTGCC<sup>1</sup>CTGCC<sup>2</sup>GTACCCG<sup>3</sup>AGACAGCC<sup>4</sup>CTGCC<sup>5</sup>CTCC<sup>6</sup>CTGACCCGCC<sup>7</sup>AGC<sup>8</sup>AGGCC<sup>9</sup>CTG<sup>10</sup>C<sup>11</sup>  
 ALE<sup>12</sup>LEU<sup>13</sup>PRO<sup>14</sup>ALA<sup>15</sup>ALA<sup>16</sup>LEU<sup>17</sup>VAL<sup>18</sup>ILE<sup>19</sup>SER<sup>20</sup>PHE<sup>21</sup>LEU<sup>22</sup>LEU<sup>23</sup>GLY<sup>24</sup>LEU<sup>25</sup>GLY<sup>26</sup>LEU<sup>27</sup>VAL<sup>28</sup>ALA<sup>29</sup>CY<sup>30</sup>  
 TM-----\* (1080)

FIG. 8A

TGTGCTGGCGAGGACACAGATAAAGAAACTGTGCTCGTGGCGGATAAGAATTGGCGGC (1140)  
SVALLEUALAARGTHRLNILELYSLEUCYSSETRPARGASPLYSASN SERALAAL  
-----  
ATGTGTGGTGTACGAGGACATGTGCAACAGCGCTGCAAACGCTGTCTCCCCAACCA (1200)  
ACYSVALVALTYRGLUASPME SERHISSE RARGCYSASNTHRLEUSERSERPROASNGL  
-----  
GTACCA GTGACCCAGTGGGCCCTGCACGTCCGCCTGTGGTCCCCAACGACCTTCCCT (1260)  
NTYRGLNEND  
GCCACCACTGCCACACACCCCTCACCTGCTGCTCCACGGCTGCAG (1320)  
CAGAGTTGAAAGGGCCAGCCTGCCACACACAGGAGCTGGCCAGG (1380)  
CCCACGGTGTCTCAGTGGACAATGATGCTCCTCCGGAGCCTCCCTGCCAGCC (1440)  
ACGCCGCCACCGGGAGGAAGCCTGACTGTCTTGGCTGCACTCTCCGAACATGGCCAAG (1500)  
GAGGGCTTCTGTGGATGGCCCTGGCAACGGCCCTCTCTGTCA GTGCCGGCCACC (1560)  
CACCAGCAGGCCAACCCAGGCAGGCCAGAGGAGGGAGGAGACCAGTCCCC (1620)  
-----  
ACCCAGCCGTACCAAAATAAAGGCTTCTGTGCTCAAAAAAAAA (1665)

**FIG. 8B**

CCCAAATGTCTCAGAATGTATGTCCCAGAAACCTGTGGCTGCTCAACCATTGACAGTT (60)  
 METSERGLNASNVALCYS PROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL  
 -29  
 TGCTGCTGCTGGCTCTGCAGACAGTCAGCTGCAGCTCCCCAAAGGCTGTGCTGAAAC (120)  
 EUFULEULEUÁLASERAALÁASPSERGLNALAALAALAPROPROLYSALAVALLEULYSL  
 -1 +1  
 TTGAGCCCCGTGGATCAAACGTGCTCCAGGAGGACTCTGACTCTGACATGCCAGGGG (180)  
 EUGLUPROPROTRPILEASNVALLEUGLNLUASPVALTHRLEUTHRCYSGLNGLYA  
 \*  
 10 CTCGCAGCCCTGAGAGCGACTCCATTCACTGGTCCACAATGGAAATCTCTTCCCACCC (240)  
 30 LAARGSERPROGLUSERASP SERILEGLNTRPHEHISASNGLYASNLEUILEPROTHR (300)  
 50 ACACGCCAGCCTACAGGTTCAAGGCCAACAAATGACAGCGGGAGTACACGTGCC (360)  
 ISTHRGLNPROSERTYRARGPHLYSALAASNASNASP SERGLYGLUTYRTHRCYSG  
 ---CHO--- \*  
 70 AGACTGGCCAGACCAAGCCTCAGCGACCCCTGTGCATCTGACTGTGCTTCCGAATGGCTGG (420)  
 LNTHRGGLYGLNTHR SERLEUSERASP PROVALHISLEUTHRVALLEUSERGLUTRPLEUV  
 90 TGCTCCAGAACCCCTCACCTGGAGTTCCAGGAGGGAGAAAATCATCATGCTGAGGTGCCAC (480)  
 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRILEMETLEARGCYSHISS  
 \*  
 110 GCTGGAAGGACAAGCCTCTGGTCAAGGTCACTTCCAGAACAAACAGTCAGTGGT (540)  
 ERTRPLYSASPLYS PROLEUVALLYSVALTHR PHEGLNASNGLYLYSSERGLNLYSP  
 130 TCTCCCGTTGGATCCCACCTCTCCATCCACAAGCAAACCAACAGTCAGTGGT GATT (600)  
 HESERARGLEUASPPROTHR PHESERILEPROGLNALAASN HISERHISERGLYASPT  
 ---CHO---  
 150 ACCACTGCAAGGAAACATAGGCTACACGCTGTCTCATCCAAGCCTGTGACCATCACTG (660)  
 YRHISCYSTHRGLYASNILEGLYTYRTHRLEUPHESERSERLYSPROVALTHRILETHR  
 \*  
 170 TCCAAGTGCACAGCATGGGAGCTCTCACTCAATGGGAATCATTGTGGCTGTGGTCATTG (720)  
 ALGLNVALPROSERMETGLYSERSERSPROMETGLYILEILEVALALAVALVALILEA  
 190 CGACTGCTGAGGCCATTGGCTGCTGTAGTGGCCTGATCTACTGCAGGAAAAGC (780)  
 LATHR ALAVALALAALAI L E VALALAVALVALALALEUILETYRCYSARGLYSLYS  
 -----TM-----  
 210 GGATTTCAGCCAATTCCACTGATCCTGTGAAGGCTGCCAATTGAGCCACCTGGACGT (840)  
 RGILESERALASN SERTHRASP PROVALYSALAALAGLN PHEGLUPROPROGLYARGG  
 230 AAATGATTGCCATCAGAÁAGAGACAACCTGAAAGAAACCAACAAATGAAACAGCTG (900)  
 LN METILEALAI L E ARGGLYSARGGLNLEUGLUGLUTHRASNASNASP TYRGLUTHR ALA  
 250 ACGGGGGCTACATGACTCTGAAACCCAGGGCACCTACTGACCATGATAAAACATCTACC  
 SPGLYGLYTYR METTHRLEUASN PROARGALAPROTHRASPASPLYSASNILETYRL

FIG. 9-A

270 TGACTCTCCCAACGACCATGTCAACAGTAATAACTAAAGAGTAACGTTATGCCATG (960)  
 EUTHRLEUPROPROASNPHISVALASNERSASNEND  
 282 TGGTCATACTCTCAGTTGCTGAGTGGATGACAAAAAGAGGGATTGTTAAAGGAAAAT (1020)  
 TTAAATGGAGACTGGAAAATCCTGAGCAAAACCACTGGCCCTTAGAAATAGCTT (1080)  
 TAACTTTGCTAAACTACAAACACAAGCAAAACTCACGGGGTACTACATACAAGCA (1140)  
 TAAGCAAAACTTAACCTGGATCATTCTGTTAAATGCTTATGTTAGAAATAAGACAACCC (1200)  
 CAGCCAATCACAAGCAGCTACTAACATAATTAGGTGACTAGGGACTTCTAAGAAGA (1260)  
 TACCTACCCCAAAAAACAATTATGTAATTGAAAACCAACCGATTGCCCTTATTTGCTT (1320)  
 CCACATTTCCTAAATACCTGCCTGTGACATTGCTTACTGGAACACTAAACTTCAT (1380)  
 GAATTGCGCCTCAGATTTCTTAAACATCTTTTTTTGACAGAGTCTCAATCTG (1440)  
 TTACCCAGGCTGGAGTGCAGTGGTGCTATCTGGCTACTGCAAACCCGCTCCAGGT (1500)  
 TAAGCGATTCTCATGCCTCAGCCTCCAGTAGCTGGATTAGAGGCATGTCGCATCATA (1560)  
 CCAGCTAATTGGTATTATTATTATTATTAGTAGAGACAGGGTTTCCGAATGTT (1620)  
 GGCCAGGCCGATCTGAACCTCTGGCTCTAGCGATCTGCCGCTCGGCCCTCCCAAAGT (1680)  
 GCTGGGATGACCAGCATCAAGCCCAATGTCCAGCCTCTTAAACATCTCTTCCATGCT (1740)  
 CTCTCTGGATCCCTACTGCTGGTTCTGCCCTCCATGCTGAGAACAAATCACCTA (1800)  
 TTCACTGCTTATGCAGTCGGAAGCTCCAGAAGAACAAAGAGCCAATTACAGAACAC (1860)  
 TTAAGCTCTCATTGTTTGCCCTGGGATTGAGAAGAGAATTAGAGAGGTGAGGATCTGG (1920)  
 TATTCTGGACTAAATTCCCTTGGGAAGACGAAGGGATGCTGCAGTCCAAAGAGA (1980)  
 AGGACTCTCAGAGTCATCACCTGACTCCAAAGCTCCTGCTGAAAGCCACAGAC (2040)  
 AATATGGTCCTAAATGACTGACTGCACCTCTGTGCCTCAGCCGTTCTGACATCAAGAA (2100)  
 TCTTCTGTTCCACATCCACACAGCCAATACAATTAGTCACCAACTGTTATTAAACAGATG (2160)  
 TAGCAACATGAGAACGCTTATGTTACAGGTTACATGAGACCAATCATGTAAGTCTATA (2220)  
 GACTTCAGAAATGTTAAAATAGACTAACCTCTAACAAACAAATTAAAGTGTATTGTTCAA (2280)  
 GGTGAAAAAA (2290)

**FIG. 9-B**

1 CTCAGGCCCTATGGCTCCAGGCCAGCCCCGGCTGCCGCACTCTGGTCTGCTGGGCTCTGTTCCCA  
Met Ala Pro Ser Ser Pro Arg Pro Ala Leu Pro Ala Leu Val Leu Val Leu Pro  
(-25)

GGACCTGGCAAATGCCAGACATCTGTCTCCCCCTCAAAAGTC  
Gly Pro Gly Asn Ala Gln Thr Ser Val Ser Pro Ser Lys Val  
(+11)

121 ATCCCTGCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCTGTGACCCAGGCCAAGCTTGTGGCATAGAGACC  
Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys Ser Thr Ser Cys Asp Gln Pro Lys Leu Val Ile Glu Thr  
(+1)

CCGTTGCCCTAAAGGAGGTTGCTCGCCTGGCTGGAAACACCCGG  
Pro Leu Pro Lys Lys Glu Leu Leu Pro Gly Asn Asn Arg  
(+61)

241 AAGGTGTATGAACTGAGCAATGTGCAAGAAGATAAGCCAACTGCCCCTGATGGGCAGTCACAA  
Lys Val Ile Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys Pro Asp Gln Ser Thr  
GCTAAACCTTCCTCACCGTGTACTGGACTCCAGAACGGCTG  
Ala Lys Thr Phe Leu Thr Val Ile Tyr Trp Thr Pro Glu Arg Val  
(+91)

361 GAACTGGCACCCCTCCCTGGCAGCCAGTGGCAAGAACCTTACCCCTAACGCTGCCAGGTGGAGGGCACCC  
Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Lys Ala Pro  
---CHO---

CGGCCAACCTCACCGTGGTGGCTCCGTGGGAGAAGGAG  
Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu  
(+131)

481 CTGAAACGGAGGCCAGCTGTGGGGAGCCGACACGGTGCTGGTGAAGGAGAGATCACCATGGAGCC  
Leu Lys Arg Glu Pro Ala Val Ile Gly Glu Pro Ala Val Ile Val Thr Thr Val Val Leu Val Arg Arg Asp His Glu Ala  
AATTTCCTGGTGGCACTGGACCTGGGGCCCCAAGGG  
Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu Arg Pro Glu Gly  
---CHO---  
(+171)

801 CTGGAGCTGTTTGAGAACACCTCGGGCCCTACCAAGCTCCAGAACCTTGTGCTGCCAGCGACTCCCCAACACTTGTCT  
Leu Glu Leu Pro Val Gln Thr Ser Ala Pro Tyr Gln Leu Val Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val  
---CHO---  
(+211)

AGCCCCGGGTCTAGGGTGGACACGGCAGGGACCCGGTC  
Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val  
(+211)

FIG. 11-A

721 TGTTCCCTGACGGGGCTGTTCCAGTCTCGGACCTGGCACTGGGACCCAGGGCCAGGGTGTGAAACCCACA  
 CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr  
 GTCACCTATGGCAACGACTCCCTCTGGCCAAAGGCCAGCTCAGTC  
 ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal  
 ---CHO---  
 (+251)

841 AGTGTGACCGAGGGACGGCACCCAGGGCTGACCTGAGCTTAATACTGGGAAACCAGAGCCAGGAGACACTG  
 SerValThrAlaGluAspGlyAspGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu  
 ---CHO---  
 CAGACAGTGAACCATCTACAGCTTCCGGCCAACGTCATT  
 GlnThrValThrIleTyrSerPheProAlaProAsnValIle  
 (+291)

961 CTGACGAAGGCCAGAGGTCTCAGAAAGGACCCAGGGTGTGACAGTGAAGTGTGAGGCCACCCCTAGAGCCAAAGGTGACGGCTG  
 LeuThrLysProGluValSerGluValSerValIleGlyThrValIleGlyThrValIleGlyAsnGluAlaHisProArgAlaLysValThrLeu  
 AATGGGGTTCCAGGCCAGGCCACTGGGCCAGGGCCAGCTC  
 AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu  
 (+331)

1081 CTGCTGAAGGCCACCCAGAGGACAACGGGCCAGCTCTCTGCTCTGCTCTGCAACCTGGAGGTGGCCAGGCTTATA  
 LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle  
 CACAAGAACCCAGACCCGGAGCTTCTGTCCTGTATGGCCCC  
 HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro  
 ---CHO---  
 (+371)

1201 CGACTGGACGAGGGATTGTCCGGAAACTGGACGTTGGCCAGAAAATTCCCAGCAGACTCCAAATGTGCCAGGCTTGG  
 ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnGlnSerGlnAlaTrp  
 ---CHO---  
 GGGAAACCCATTGGCCCGAGGCTCAAGTGTCTAAAGGATGGCACT  
 GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr  
 (+411)

1321 TTCCCCACTGCCCATCGGGGAATCAGTGACTGTCAGTGACCTGGCCACCTACCTCTGTCGGGCCAGGAGGCACT  
 PheProLeuProIleGlyGluValSerValThrArgAspLeuGlyThrTyrLeuCysArgAlaArgSerThr  
 CAGGGGAGGTCAACCCGGAGGTGACCGTGAATGTGCTCTCC  
 GlnGlyGluValThrArgGluValThrValAsnValLeuSer  
 (+451)

FIG. 11-B

FIG. 11-C

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT  
51 CTTCCTCACC CCCATGGAAG TCAGGCCCCA GGAACCTCTA GTGGTGAAGG  
101 TGGAAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT  
151 GQCCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCCTT  
201 CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGGATCCAC ATGAGGGCCCC  
251 TGGCCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC  
301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG  
351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG  
401 ACCTAGGTGG CCTGGCTGT GGCCTGAAGA ACAGCTCCTC AGAGGGCCCC  
451 AGCTCCCCTT CCGGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA  
501 AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG  
551 ACAGCCTGAA CAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC  
601 ACACTCTGGC TGTCTGTGG GGTACCCCT GACTCTGTGT CCAGGGGCC  
651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC  
701 TAGAGCTGAA GGACGATCGC CCGGCCAGAG ATATGTGGT AATGGAGACG  
751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGAA AGTATTATTG  
801 TCACCGTGGC AACCTGACCA TGTCAATTCCA CCTGGAGATC ACTGCTCGGC  
851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT  
901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTTCCCTTG TGGCATTCT  
951 TCATCTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG  
1001 ACCCCACCAAG GAGATTCTTC AAAGTGACGC CTCCCCCAGG AAGCGGGCCC  
1051 CAGAACCAAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT  
1101 CGGACGGGCC CAGCGTTGGG CCGCAGGCCT GGGGGGACT GCCCCGTCTT  
1151 ATGGAAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGGTCCCCG

**FIG. 12-A**

1201 AGCCGCCGGG AGTGGGCCA GAAGAAGAGG AAGGGAGGG CTATGAGGA  
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG  
1301 GCAGGACCAAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG  
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT  
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTGCCAGGA CAATGGACTT  
1451 CCTGAGCCCT CATGGTCAG CCTGGGACCC CAGCCGGAA GCAACCTCCC  
1501 TGGGGTCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC  
1551 CAQCTCCGCT CCATTGGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC  
1601 AGACTCTTAT GAGAACATGG ATAATCCGA TGGGCCAGAC CCAGCCTGGG  
1651 GAGGAGGGGG CCGCATGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC  
1701 CAGCCTGGAT CTCCTCAAGT CCCCAGATT CACACCTGAC TCTGAAATCT  
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT  
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGT GTGTGTGT GTGTGTGT  
1851 ATACATGCCA GTGACACTTC CAGTCCCCCTT TGTATTCCCTT AAATAAAACTC  
1901 AATGAGCTCT TCCAAAAAAA AAAA

**FIG. 12-B**

1 ACAAAGACAA ACTGCACCCA CTGAACCTCG CAGCTAGCAT CCAAATCAGC  
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTGAGA GCAAAATGAC  
101 AACACCCAGA AATTCAAGTAA ATGGGACTTT CCCGGCAGAG CCAATGAAAG  
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT  
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT  
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC  
301 TTCTGATGAT CCCACCGAGG ATCTATGCAC CCATCTGTGT GACTGTGTGG  
351 TACCCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC  
401 AGCAACGGAG AAAAACTCCA GGAAGTGTGTT GGTCAAAGGA AAAATGATAA  
451 TGAATTCAATT GAGCCTCTTT GCTGCCATT CTGGAATGAT TCTTTCAATC  
501 ATGGACATAC TTAATATTAA AATTCCCATT TTTTTAAAAA TGGAGAGTCT  
551 GAATTTTATT AGAGCTACA CACCATATAT TAACATATAC AACTGTGAAC  
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC  
651 ATACAATCTC TGTTCTGGG CATTGGTCA GTGATGCTGA TCTTTGCCCTT  
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA  
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA  
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGC TAACTGAAAC  
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG  
901 AAGAGGAAGA AGAAAGAAACA GAGACGAAC TTCCAGAACCC TCCCCAAGAT  
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC  
1001 TGTTTTCTGT TTCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC  
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

**FIG. 13-A**

1101 ATCTGGCCTT TGCATGGAGT GACCATAAGCT CCTTCTCTCT TACATTGAAT  
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTACGC TTCTTCTTTT  
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG  
1251 ATTTCTACT AACCTGTTCC TTGGATAGGC TTTTTAGTAT AGTATTTTTT  
1301 TTTGTCATTT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG  
1351 ATATATGACT GCTTCATGAC ATTCCCTAAC TATCTTTTTT TTATTCCACA  
1401 TCTACGTTTT TGGTGGAGTC CCTTTTATC ATCCTAAAAA CAATGATGCA  
1451 AAAGGGCTTT AGAGCACAAT GGATCT

**FIG. 13-B**

1 CCCAAATGTC TCAGAATGTA TGTCAGAA ACCTGTGGCT GCTTCAACCA  
51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC  
101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG  
151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGGAC  
201 TCCATTCACT GGTTCCACAA TGGAATCTC ATTCCCACCC ACACGCAGCC  
251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC  
301 AGACTGGCCA GACCAGCCTC AGCGACCTG TGCATCTGAC TGTGCTTTCC  
351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTCCAGG AGGGAGAAC  
401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA  
451 CATTCTCCA GAATGGAAAA TCCCAGAAAT TCTCCGTTT GGATCCCACC  
501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC  
551 AGGAAACATA GGCTACACGC TGTTCATC CAAGCCTGTG ACCATCACTG  
601 TCCAAGTGCC CAGCATGGGC AGCTCTTCAC CAATGGGGAT CATTGGCT  
651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT  
701 GATCTACTGC AGGAAAAAGC GGATTCAGC CAATTCCACT GATCCTGTGA  
751 AGGCTGCCA ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG  
801 AGACAACCTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCCGCTA  
851 CATGACTCTG AACCCAGGG CACCTACTGA CGATGATAAA AACATCTACC  
901 TGACTCTCC TCCCACGAC CATGTCACCA GTAATAACTA AAGAGTAACG  
951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG ACAAAAAGAG  
1001 GGGATTGTT AAAGGAAAT TTAAATGGAG ACTGGAAAAA TCCTGAGCAA  
1051 ACAAAACAC CTGGCCCTTA GAAATAGCTT TAACTTGCT TAAACTACAA  
1101 ACACAAGCAA AACTTCACGG GGTCTACTA CATAACAAGCA TAAGCAAAAC  
1151 TTAACCTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC  
1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT  
1251 TCTAAGAAGA TACCTACCCC CAAAAAACAA TTATGTAATT GAAAACCAAC  
1301 CGATTGCCCTT TATTTGCTT CCACATTTTC CCAATAAATA CTTGCTGTG  
1351 ACATTTGCC ACTGGAACAC TAAACTTCAT GAATTGCGCC TCAGATTTT  
1401 CCTTTAACAT CTTTTTTTTT TTGACAGAG TCTCAATCTG TTACCCAGGC  
1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGTT  
1501 TAAGCGATT TCATGCCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT  
1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTT TTTTAGTAG  
1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT  
1651 AGCGATCTGC CGCCCTCGGC CTCCCCAAAGT GCTGGGATGA CCAGCATCAG

**FIG. 14-A**

1701 CCCCAATGTC CAGCCTCTTT AACATCTTCT TTCTATGCC CTCTCTGTGG  
1751 ATCCCTACTG CTGGTTCTG CCTTCTCCAT GCTGAGAACAA AAATCACCTA  
1801 TTCACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAAGA GCCCAATTAC  
1851 CAGAACACAA TTAAGTCTCC ATTGTTTGC CTTGGGATTT GAGAAGAGAA  
1901 TTAGAGAGGT GAGGATCTGG TATTTCTGG ACTAAATTCC CCTTGGGAA  
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGACTCATC  
2001 TACCTGAGTC CCAAAGCTCC CTGTCTGAA AGCCACAGAC AATATGGTCC  
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTT ACATCAAGAA  
2101 TCTTCTGTTC CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA  
2151 TTAACAGATG TAGAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA  
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAAT AGACTAACCT  
2251 CTAACAAACAA ATTAAAAGTG ATTGTTCAA GGTGAAAAAA

**FIG. 14-B**

1 GCTGTGACTG CTGTGCTCTG GGCGCCACTC GCTCCAGGGGA GTGATGGGAA  
51 TCCTGTCACTT CTTACCTGTC CTTGCCACTG AGAGTGACTG GGCTGACTGC  
101 AAGTCCCCCCC AGCCTTGGGG TCATATGCTT CTGTGGACAG CTGTGCTATC  
151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCCAAAG GCTGTGCTGA  
201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG  
251 ACATGCCGGG GGACTCACAG CCCTGAGAGC GACTCCATTG AGTGGTTCCA  
301 CAATGGGAAT CTCATTCCCA CCCACACCGCA GCCCAGCTAC AGGTTCAAGG  
351 CCAACAAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC  
401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC  
451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA  
501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG  
551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCTCTAGT TCTGATTGAA  
601 CAGAAGAAGG TTTCAAGGCC AAAAACAGGC AGCCAAGTGT GAGAGAAGCA  
651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTAA TGGCAGAATT  
701 GAAAAGCACA GACCACAACG GAATCCTAGC CCTGAAATG ACTCACTATA  
751 CAACATGATG AATTCAATTAA ACCCTTGAGT TTCCATTCTC TCACCTGTC  
801 CGTGGGGCAG TAACGCCCTC CTCAGAGGCT TCTGGTGAGA ATCACTGTT  
851 CCCTGCCCTC GCCCCGCCCT CCATGCCCT TCTCCACGTT CTCACTGTC  
901 TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG  
951 ATGAAAGTCG TGTCTTACCC ATCTTGTAT TTCCAGCATC TGAAACTGGG  
1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC  
1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAAAG GTTACAATGA GATTGTGATG  
1101 AACATTGTCC TTGTGGCTTT TCACCTAGTC CCCTCCCTTC ACCTGAACAG  
1151 CAAATTTC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT  
1201 GTTGCCTTA GACCCTGCTG GAAAGAAGCT CCACATTAT TAACATTCCC  
1251 GAAGTAAATT TATCAGGTAG CATTGATCAG GTAACATTG TTGCACATTG  
1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCTTATCA TATGCCACT  
1351 CCTCGGTAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC  
1401 ATCTTAGGGT CTCTGTGTT CTTCCCTGAG AGGCCTGTGG GGCAGGAAAA  
1451 GGCTGCAGCT GCCTTCCCTGG GAGAAGGAGG AGATGAGTGT ATCCTGAACA  
1501 CCTATTATGT GCTAGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT  
1551 TTTCACGAAT GAGGAAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA  
1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTCA  
1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCCAGTA AGGAAGATCT

FIG. 15-A

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCCTCGCG GTTTTTGTG  
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG  
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC  
1851 AAGGTACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCGGA  
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC  
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC  
2001 ATCACTGTCC AAGCTCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT  
2051 GGTCACTGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA  
2101 TCTACTGCAG GAAAAAGCGG ATTTCAAGGTT TGTAGCTCCT CCCGGTCCCT  
2151 TTTGTTATCA GTTTCCACTT T

**FIG. 15-B**

1 GCCTCGCTCG GGCGCCAGT GGTCCCTGCCG CCTGGTCTCA CCTGCCATG  
51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT  
101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACAA  
151 GTCAGTGCCTG TTCTTGTGC CAGCCAGGAC AGAAACTGGT GAGTGACTGC  
201 ACAGAGTTCA CTGAAACGGA ATGCCCTCCT TGGCGTGAAA GCGAATTCT  
251 AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC  
301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC  
351 ATCTGCACT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG  
401 CTGTGTCTG CACCGCTCAT GCTCGCCCGG CTTGGGGTC AAGCAGATTG  
451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCAGT CGGCTCTTC  
501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCCTTGGA CAAGCTGTGA  
551 GACCAAGAC CTGGTTGTGC AACAGGCAGGC ACAAAACAAGA CTGATGTTGT  
601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT  
651 TCGGGATCCT GTTGCCATC CTCTTGGTGC TGGCTTTAT CAAAAACGTG  
701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA  
751 GATCAATTT CCCGACGATC TTCTGGCTC CAACACTGCT GCTCCAGTGC  
801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG  
851 AGTCGCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT  
901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC  
951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCAAGTCA GTGCCAGCCC  
CTC

**FIG. 16**